

Supplementary Figure 6

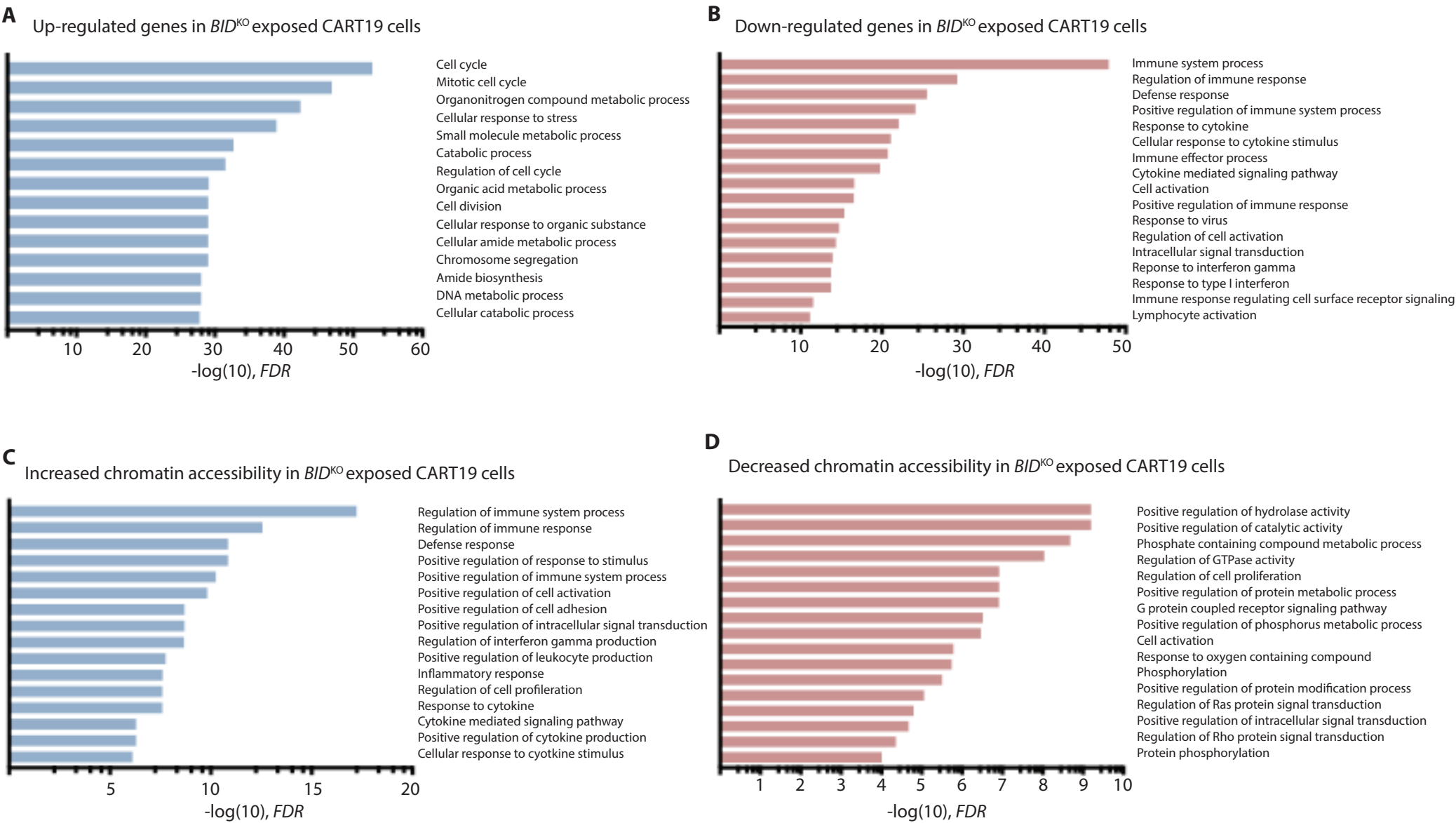


Figure S6. GSEA of transcriptomic and epigenomic sequencing of CART19 cells exposed to either WT or BIDKO Nalm6.
(A-D) CART19 cells were exposed to Nalm6 cells for 15 days and underwent RNA sequencing or ATAC sequencing. Sequenced gene transcripts or promoter sites found to be significantly different ($FDR < 0.05$, \log -fold change > 0.5) were analyzed using gene ontology (GO) pathway terms to identify pathways that were (A) up-regulated, (B) down-regulated, (C) more-accessible, or (D) less-accessible in BIDKO exposed CART19 cells.